



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 113842

TO: Minh-Tam Davis  
Location: Rem 3a24 / 3c18  
Tuesday, February 10, 2004  
Art Unit: 1642  
Phone: 272-0830  
Serial Number: 10 / 032159

From: Jan Delaval  
Location: Biotech-Chem Library  
Rem 1A51  
Phone: 272-2504

jan.delaval@uspto.gov

### Search Notes

*priority date 12/2000*

STIC-Biotech/ChemLib

113 842

From: Chan, Christina  
Sent: Monday, February 09, 2004 10:11 AM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 10/032159

RECEIVED  
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STIC/BIOTECH/CHM. LIB.  
(STIC)

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Sunday, February 08, 2004 11:02 AM  
To: Chan, Christina  
Subject: Rush search request for 10/032159

Please search in commercial database, issued patent files, PGPUB and interference:  
SEQ ID NO:17, and 18, with and without size limitation to the size of the corresponding sequence.  
Thank you.

MINH TAM DAVIS  
ART UNIT 1642,  
RESEM, ROOM 3A24, mb 3c18  
272-0830

Searcher: Jan  
Phone: 22504  
Location: \_\_\_\_\_  
Date Picked Up: 2/9  
Date Completed: 2/6  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: W  
Online time: W

TYPE OF SEARCH: ☒  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: ☒  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

PS Claim 9; Fig 14A-14C; 145pp; English.

CC The present sequence represents novel human caspase recruitment  
CC domain, CARD-11. The polynucleotide encoding this sequence was  
CC isolated from a human T-cell cDNA library. Also described are  
CC novel human sequences for CARD-9 and CARD-10 (AA001205, AA001206)  
CC and rat CARD-9 (AA001204). CARD-9, CARD-10 and CARD-11 interact  
CC with Bcl-10 which is thought to activate nuclear factor (NF)-kappaB  
CC and apoptosis. The sequences of the invention can be used for  
CC treating a disorder associated with abnormal levels of apoptosis by  
CC modulating the expression or activity of CARD-9, CARD-10, or CARD-11.  
CC They can be used for the treatment of hyperproliferative disorders  
CC (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus),  
CC neurological disorders (e.g. Alzheimer's disease), inflammatory disorders  
CC (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD  
CC polypeptide, polynucleotide and an antibody which selectively binds to  
CC CARD can be used in screening and detection assays (e.g. chromosomal  
CC mapping, tissue typing), predictive medicine (prognostic assays,  
CC monitoring clinical trials, and therapy (treatment and prophylaxis). The  
CC CARD polypeptide may be used to screen for drugs that bind to and/or  
CC modulate it. CARD sequences are potential targets for regulating  
CC inflammation, cancer, NF-kappaB signalling, stress-related response and  
CC apoptosis in human disease. A host cell containing a polynucleotide  
CC encoding CARD can be used to create transgenic animals.

XX  
XX  
SQ Sequence 1147 AA;

QY 1 EETLWEMESHRRIRYACIPSKLPTLRQAKVLCQDESEVYLSHPSLTSNMAAGHLD 60  
QY 12 EDALWVEWECNRRHLSRYINPAKLPYLRCKXYIDCEDDEVINAPMLPSKINRAGRLLD 71  
QY 61 LKTRGNAGAIAPLESIKFHNPDVYLVTG 90  
QY 72 LKTKGGRGVFPLESLSEFYPELVKLVTG 101  
Db

RESULT 5  
AAG79555  
ID AAG79555 standard; Protein: 1147 AA.  
XX AAG79555;  
XX  
DT 09-DEC-2002 (first entry)  
XX  
XX Human CARD-11.  
DE  
XX  
XX Rat; human; caspase recruitment domain; CARD-9; CARD-10;  
KW CARD-11; apoptosis; inflammation; cell growth; cell death;  
KW lymphocyte activation; cancer; melanoma; autoimmune disease;  
KW arthritis; neurological disorder; Alzheimer's disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key location/Qualifiers  
XX FH 6..112  
XX FT Domain /label= CARD\_domain  
XX FT Domain 130..431 /label= CARD-coiled-coil\_domain  
XX FT Domain 635..748 /label= PDZ\_domain  
XX FT Domain 766..834 /label= SH3\_domain  
XX FT Domain 882..1147 /label= Guanylate\_kinase\_domain  
XX FT Domain 635..1147 /label= MAGUK\_domain  
XX  
XX W0200270652-A2.



[illegible]

FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	570..573
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	595..598
FT	Modified-site	/note= "N-glycosylation site"
FT	Modified-site	603..605
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	638..641
FT	Modified-site	/note= "Glycosaminoglycan attachment site"
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FT	Modified-site	714..717
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	733..739
FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
FT	Modified-site	748..751
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FT	Modified-site	754..756
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	754..757
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FT	Modified-site	761..766
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FT	Modified-site	809..814
FT	Modified-site	/note= "N-myristoylation site"
FT	Domain	
FT	Modified-site	830..1032
FT	Modified-site	/note= "Guanylate kinase (GUK) domain"
FT	Modified-site	830..832
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	868..870
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	869..872
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FT	Modified-site	882..885
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FT	Modified-site	893..898
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	915..918
FT	Modified-site	/note= "Amdation site"
FT	Modified-site	947..949
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	981..986
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FT	Modified-site	1021..1026
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	1022..1024
FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1028..1031
FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FN	WO200140468-A2.	
PD	07-JUN-2001.	
XX	01-DEC-2000; 2000WO-US32716.	
XX	03-DEC-1999; 99US-0166780.	
XX	18-FEB-2000; 2000US-0507533.	
XX	25-FEB-2000; 2000US-0513904.	
XX	10-OCT-2000; 2000US-0685791.	

PA (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J;  
 PI  
 XX WPI; 2001-367809/78.  
 DR N-PSDB; AAS05386.  
 XX  
 PT Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10,  
 PT CARD-11, useful as targets for therapy, as immunogens, and in screening  
 PT and detection assays -  
 XX  
 PS Claim 9; Fig 10A-10C; 145bp; English.  
 XX  
 CC The present sequence represents novel human caspase recruitment  
 CC domain, CARD-10. The polynucleotide encoding this sequence was isolated  
 CC from a human skin cDNA library. Also described are novel human sequences  
 CC for CARD-9 and CARD-11 (AAU01205, AAU01207) and rat CARD-9 (AAU01204).  
 CC CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which is thought to  
 CC activate nuclear factor (NF)-kappaB and apoptosis. The sequences of the  
 CC invention can be used for treating a disorder associated with abnormal  
 CC levels of apoptosis by modulating the expression or activity of CARD-9,  
 CC CARD-10, or CARD-11. They can be used for the treatment of  
 CC hyperproliferative disorders (e.g. cancer), autoimmune disorders (e.g.  
 CC systemic lupus erythematosus), neurological disorders (e.g.  
 CC Alzheimer's disease), inflammatory disorders (e.g. Crohn's disease),  
 CC and viral infection (e.g. HIV). The CARD polypeptide, polynucleotide  
 CC and an antibody which selectively binds to CARD can be used in screening  
 CC and detection assays (e.g. chromosomal mapping, tissue typing),  
 CC predictive medicine (prognostic assays, monitoring clinical trials, and  
 CC therapy (treatment and prophylaxis). The CARD polypeptide may be used  
 CC to screen for drugs that bind to and/or modulate it. CARD sequences are  
 CC potential targets for regulating inflammation, cancer, NF-kappaB  
 CC signalling, stress-related response and apoptosis in human disease. A  
 CC host cell containing a polynucleotide encoding CARD can be used to  
 CC create transgenic animals.  
 CC  
 SQ Sequence 1032 AA;  
 QY  
 Db 1 EETLWMMESHRRIRIVICIPSRITPYLRQAKVLCQDDEEVVLSHSPRLTMSAMRAGHLLD 60  
 24 EDALMERIEGVRHRIALPALNPACTLPYLRQCRVIDDEDEEVVLSYRPPCRVNRKRLMD 83  
 QY 61 LLKTRGKNGAIAFLPSLKFNPDVYTLVTG 90  
 84 ILRCRGKRGYEAFLPSLFFYPHFTLLTG 113  
 Db  
 RESULT 8  
 AAG79554  
 ID AAG79554 standard; Protein; 1032 AA.  
 XX  
 AC AAG79554;  
 XX  
 DT 09-DEC-2002 (first entry)  
 XX  
 DE Human CARD-10.  
 XX  
 KW Rat; human; caspase recruitment domain; CARD-9; CARD-10;  
 KW CARD-11; apoptosis; inflammation; cell growth; cell death;  
 KW lymphocyte activation; cancer; melanoma; autoimmune disease;  
 KW arthritis; neurological disorder; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 23..123  
 FT Domain /label= CARD\_domain  
 FT 147..457  
 FT Domain /label= Coiled-coil\_domain

FT Domain 704..772  
 FT /label= SH3\_domain  
 FT 830..1032  
 FT Domain /label= Guanylate\_kinase\_domain  
 FT 366..398  
 FT Domain /label= Tropomyosin\_domain  
 FT 457..1032  
 FT Domain /label= MAGUK\_domain  
 PN W0200270652-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 XX 28-FEB-2002; 2002W0-US06147.  
 XX  
 XX 02-MAR-2001; 2001US-0798412.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J;  
 PI  
 XX WPI; 2002-698749/75.  
 DR N-PSDB; ABA00333.  
 XX  
 PT CARD-9, CARD-10 or CARD-11 polypeptides and polynucleotides, useful for  
 PT treating disorders associated with inappropriate apoptosis or  
 PT lymphocyte activation, e.g. cancer -  
 XX  
 PS Claim 14; Fig 10; 151bp; English.  
 XX  
 CC This sequence represents human caspase recruitment domain (CARD)-10.  
 CC CARD proteins play roles in apoptotic and inflammatory signalling  
 CC pathways. CARD-9, -10 and -11 participate in the network of  
 CC interactions that modulate caspase activity. They are thought to be  
 CC useful as modulating agents for regulating a variety of cellular  
 CC processes including cell growth and cell death. CARD proteins and  
 CC nucleic acids are useful for treating a disorder associated with  
 CC inappropriate apoptosis or lymphocyte activation or for diagnosing  
 CC subjects having or that are at risk of developing a disorder associated  
 CC with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such  
 CC as cancer e.g. melanoma, autoimmune disorders e.g. arthritis, or  
 CC neurological disorders e.g. Alzheimer's disease.  
 CC  
 SQ Sequence 1032 AA;  
 QY  
 Db 1 EETLWMMESHRRIRIVICIPSRITPYLRQAKVLCQDDEEVVLSHSPRLTMSAMRAGHLLD 60  
 24 EDALMERIEGVRHRIALPALNPACTLPYLRQCRVIDDEDEEVVLSYRPPCRVNRKRLMD 83  
 QY 61 LLKTRGKNGAIAFLPSLKFNPDVYTLVTG 90  
 84 ILRCRGKRGYEAFLPSLFFYPHFTLLTG 113  
 Db  
 RESULT 9  
 AAU73247  
 ID AAU73247 standard; Protein; 1032 AA.  
 XX  
 AC AAU73247;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human plakoglobin interacting protein #3.  
 XX  
 KW Human; plakoglobin; cytosolic; osteopathic; dermatological; cardiac;  
 KW plakoglobin related disease; skin carcinoma; acantholytic disease;  
 KW basal cell carcinoma; squamous cell carcinoma; Naxos disease;  
 KW extramammary Paget's disease; heart disease; skin blistering;  
 KW subcorneal acantholysis; Grover's disease; Halley-Halley's disease;

KM Darier's disease; ectodermal dysplasia; skin fragility syndrome.  
 XX Homo sapiens.  
 OS  
 XX WO200185933-A2.  
 PN  
 XX 15-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-EP04872.  
 PF  
 XX 09-MAY-2000; 2000EP-0201668.  
 PR  
 XX (VIAA-) VIAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 PA  
 XX Van Roy F, Bonne S, Vanlandeschoot A;  
 PI  
 XX WPI; 2002-062246/08.  
 DR  
 XX N-PSDB; AAS98203.  
 DR  
 XX New polypeptide, useful for treating skin carcinoma or acantholytic  
 PT disease such as Grover's and Darier's disease, comprises a protein  
 PT interacting with human plakoglobin and involved in transduction of  
 PT plakoglobin related signal to nucleus -  
 PT  
 XX Claim 1; Figure 3; 98p; English.  
 PS  
 XX The invention relates to an isolated plakoglobin interacting polypeptide  
 CC (1). (1) is useful as a medicament and in the manufacture of a  
 CC medicament for treating plakoglobin related diseases, such as skin  
 CC carcinoma or an acantholytic disease, and to screen compounds that  
 CC interfere with the interaction of the polypeptide with plakoglobin  
 CC The plakoglobin related diseases include basal cell carcinoma, squamous  
 CC cell carcinoma, extramammary Paget's disease, Naxos disease, heart  
 CC diseases, skin blistering and acantholytic diseases such as subcorneal  
 CC acantholysis, Grover's disease, Hailey-Hailey's disease or Darier's  
 CC disease, and ectodermal dysplasia/skin fragility syndrome. AAU73245-  
 CC AAU73254 represent novel human plakoglobin interacting protein  
 CC amino acid sequences and related sequences of the invention.  
 CC  
 XX Sequence 1032 AA;  
 SQ  
 Query Match 49.0%; Score 237; DB 23; Length 1032;  
 Best Local Similarity 50.0%; Pred. No. 1.5e-22;  
 Matches 45; Conservative 19; Mismatches 26; Indels 0; Gaps 0;  
 Qy 1 ESTLWEMESHRRHIVRCIPSRILTPYLRQAKVLCQIDEEVHLSPTLTSAMKAGHLLD 60  
 Db 24 EDALMERIEGVRRHRLARLNPAKLTPIYLRQCRVIDEDDEEVLSITYFPCKRVKRTGRLLMD 83  
 Qy 61 LLKTRGKNGALAFLESLEKFNHPDVTYTLVTG 90  
 Db 84 ILRCRGRKGYEAFLEALEFYYPHFHTLLTG 113

RESULT 10  
 AAU01204  
 ID AAU01204 standard; Protein; 536 AA.  
 XX  
 XX AAU01204;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Rat caspase recruitment domain, CARD-9 polypeptide.  
 XX  
 KM Rat; caspase recruitment domain; CARD-9; Bcl-10; NF-kappaB;  
 KM apoptosis; hyperproliferative disorder; autoimmune; neurological;  
 KM inflammatory disorder; viral infection; stress-related response.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 2.5  
 FT /note= "Casein kinase II phosphorylation site"

FT Domain  
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 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 12..15  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 16..18  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 23..26  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 92..95  
 FT /note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"  
 FT Modified-site 95..97  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 95..98  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 138..140  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 138..141  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Domain 140..416  
 FT /note= "Coiled coil domain"  
 FT Modified-site 171..174  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 176..183  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT Region 197..213  
 FT /note= "Indole-3-glycerol phosphate synthase homology region"  
 FT Modified-site 228..231  
 FT /note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"  
 FT Modified-site 231..233  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 267..270  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Region 285..338  
 FT /note= "Cysteine rich repeat homology region"  
 FT Modified-site 303..305  
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 FT Modified-site 362..364  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 362..365  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 374..377  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 425..428  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 431..433  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 451..453  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 483..486  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 514..516  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 523..528  
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 FT Modified-site 524..527  
 FT /note= "N-glycosylation site"  
 FT Modified-site 526..529  
 FT /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 531..534  
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 XX  
 PN WO200140468-A2.  
 XX  
 XX 01-DEC-2000; 2000WO-US32716.  
 XX  
 XX 03-DEC-1999; 99US-0168780.  
 PR 18-FEB-2000; 2000US-0507533.  
 PR 25-FEB-2000; 2000US-0513904.

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FT /label= CARD_domain
```

KM antiviral; antibacterial; antifungal; antineumatic; antithyroid;  
KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KM



KM neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KM cholesterol ester storage; systemic lupus erythematosus; infection;  
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KM thrombosis; contraceptive.  
 OS Homo sapiens.  
 XX  
 XX  
 XX WC200058473-A2.  
 XX  
 XX  
 XX 05-OCT-2000.  
 XX  
 XX  
 XX 31-MAR-2000; 2000WO-US08621.  
 XX  
 XX  
 XX 31-MAR-1999; 99US-0127607.  
 XX  
 XX 02-APR-1999; 99US-0127636.  
 XX  
 XX 05-APR-1999; 99US-0127728.  
 XX  
 XX 30-MAR-2000; 2000US-0540763.  
 XX  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shinkets RA, Leach M;  
 XX  
 XX WPI; 2000-602362/57.  
 XX  
 XX N-PSDB; AAC75276.  
 XX  
 XX  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX  
 XX  
 XX  
 XX Claim 11; Page 1326; 5507pp; English.  
 XX  
 XX  
 XX AAC74446 to AAC7606 encode the proteins given in ABA40237 to ABA43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vlnary;  
 CC antiproliferative; antiparasitism; neurotropic; neuroprotective;  
 CC osteoplastic; anticonvulsant; antiallergic; immunosuppressive;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;  
 CC antidiabetic; hypotensive; dermatological; immunopreventive;  
 CC antinflammatory; antibacterial; antiviral; antifungal; antihemmatic;  
 CC antihypertoid; and antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 CC  
 XX  
 XX  
 XX Sequence 174 AA;  
 SQ  
 Query Match 41.1%; Score 199; DB 21; Length 174;  
 Best Local Similarity 45.6%; Pred. No. 1.9e-18;  
 Matches 41; Conservative 14; Mismatches 35; Indels 0; Gaps 0;  
 QY 1 EETLWEMSHRRIRVCICPSRLTPYLRQAKVLCQDDEEVLSPTLTSAMAGHLLD 60  
 DB 72 DDCNVALEGRVLTSTVDSRIPIYLRQCKVLPNDEEGLVSPNVIKRKAVGLLD 131  
 QY 61 LKTRGKNGAIAFLSLKFNPNPVTTLVTG 90  
 DB 132 ILORTGHGVAFLSLKFNPNPVTTLVTG 161  
 RESULT 13  
 ABP10782

ID ABP10782 standard; Protein; 174 AA.  
 XX  
 AC ABP10782;  
 XX  
 DT 24-JUN-2002 (first entry)  
 XX  
 DE Human ORFX protein sequence SEQ ID NO:21546.  
 XX  
 XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KM hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;  
 KM degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KM hypertension; hypothyroidism; cholesterol ester storage disease;  
 KM immune deficiency; immune disorder; infectious disease;  
 KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KM myasthenia gravis.  
 XX  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX  
 XX WC200192523-A2.  
 XX  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX  
 XX 29-MAY-2001; 2001WO-US10836.  
 XX  
 XX  
 XX 30-MAY-2000; 2000US-206132P.  
 XX  
 XX 29-AUG-2000; 2000US-228716P.  
 XX  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shinkets RA, Leach MD;  
 XX  
 XX WPI; 2002-106308/14.  
 XX  
 XX N-PSDB; ABN26534.  
 XX  
 XX  
 XX Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders -  
 XX  
 XX  
 XX  
 XX Disclosure; SEQ ID 21546; 1037pp; English.  
 XX  
 XX  
 XX The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumor, keloid, degenerative disorders, hemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantations, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX  
 XX Sequence 174 AA;  
 SQ  
 Query Match 41.1%; Score 199; DB 23; Length 174;  
 Best Local Similarity 45.6%; Pred. No. 1.9e-18;  
 Matches 41; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 1 EETLMEHSHRHRYVRCICPSRLTPYLRQAKVLCQDDEEVLSPRLTNSAMRAGHLID 60  
 DB 72 DEECNVLEGGFRVTLTSVIDPSRITPYLRQCKVLPNDDDEQVLSDPNLVIRKRVGLLD 131  
 QY 61 LKTRGKCAIAFLSLKFNPDVYTLVVG 90  
 DB 132 ILQRTGKGVAFLESLDYLPOLYKRVG 161

## RESULT 14

AB95617  
 ID AAB95617 standard; Protein; 366 AA.

AC AAB95617;  
 XX

DT 26-JUN-2001 (first entry)  
 XX

DE Human protein sequence SEQ ID NO:18328.  
 XX

KM Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX

OS Homo sapiens.  
 XX

PN EF1074617-A2.  
 XX

PD 07-FEB-2001.  
 XX

PF 28-JUL-2000; 2000EP-0116126.  
 XX

PR 29-JUL-1999; 99JP-0248036.  
 XX

PR 27-AUG-1999; 99JP-0300253.  
 XX

PR 11-JAN-2000; 2000JP-0118776.  
 XX

PR 02-MAY-2000; 2000JP-0183767.  
 XX

PR 09-JUN-2000; 2000JP-0241899.  
 XX

PA (HELI-) HELIX RES INST.  
 XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 XX

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX

DR WPI; 2001-318749/34.  
 XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 XX

PT full-length cDNAs defined in the specification, and for the detection  
 XX

PT and/or diagnosis of the abnormality of the proteins encoded by the  
 XX

PT full-length cDNAs -  
 XX

PS Claim 8; SEQ ID 18328; 2537PP + CD ROM; English.  
 XX

XX The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH16332  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX  
 XX Sequence 366 AA;  
 SQ

Query Match 41.1%; Score 199; DB 22; Length 366;  
 Best Local Similarity 45.6%; Pred. No. 5.2e-18;  
 Matches 41; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 1 EETLMEHSHRHRYVRCICPSRLTPYLRQAKVLCQDDEEVLSPRLTNSAMRAGHLID 60  
 DB 7 DEECNVLEGGFRVTLTSVIDPSRITPYLRQCKVLPNDDDEQVLSDPNLVIRKRVGLLD 66  
 QY 61 LKTRGKCAIAFLSLKFNPDVYTLVVG 90  
 DB 67 ILQRTGKGVAFLESLDYLPOLYKRVG 96

## RESULT 15

ABG76060  
 ID ABG76060 standard; Protein; 366 AA.

AC ABG76060;  
 XX

DT 09-MAY-2003 (first entry)  
 XX

DE Caspase recruitment domain containing protein, CARD-10X.  
 XX

KM CARD; caspase recruitment domain; apoptosis; cell adhesion; inflammation;  
 XX cytokine receptor signaling; cancer; glioma; carcinoma; adenocarcinoma;  
 XX CARD-containing polypeptide associated disorder; sarcoma; melanoma;  
 XX hamatoma; leukemias; lymphoma; keratinocyte hyperplasia; neoplasia;  
 XX leioid; benign prostatic hypertrophy; inflammatory hyperplasia; fibrosis;  
 XX reitendosis; allergy; arthritis; lupus; Sjogren's syndrome; sepsis;  
 XX Crohn's disease; ulcerative colitis; graft versus host disease; stroke;  
 XX abnormal cell death disease; myocardial infarction; heart failure;  
 XX neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV;  
 XX CARD-10X; caspase activator; caspase inhibitor.  
 XX

OS Unidentified.  
 XX

PN Key  
 XX

PD Location/Qualifiers  
 XX

PF 12..83  
 XX

PR /label= CARD  
 XX

PR /note= "Caspase recruitment domain. Specifically  
 XX claimed in claim 12"  
 XX

PR Domain  
 XX

PR 154..297  
 XX

PR /label= Filament domain  
 XX

PR /note= "Specifically claimed in claim 12"  
 XX

PN US2002164703-A1.  
 XX

PD 07-NOV-2002.  
 XX

PF 19-DEC-2001; 2001US-0032159.  
 XX

PR 21-DEC-2000; 2000US-257457P.  
 XX

PR (PAWL/) PAWLOWSKI K.  
 XX

PR (REED/) REED J C.  
 XX

PR (GODZIK/) GODZIK A.  
 XX

PI Pawlowski K, Reed JC, Godzik A;  
 XX

PI WPI; 2003-288137/28.  
 XX

DR N-PSDB; ABX11432.  
 XX

DR New isolated CARD-containing nucleic acids, useful for the diagnosis  
 XX and treatment of disorders with aberrant expression or activity of the  
 XX CARD-containing polypeptide, such as cancer, stroke, arthritis, heart  
 XX failure and AIDS -  
 XX

PT Claim 13; Fig 1; 34pp; English.  
 XX

XX The invention relates to an isolated nucleic acid molecule encoding a  
 CC caspase recruitment domain (CARD) containing polypeptide. CARD containing  
 CC polypeptides are involved in apoptosis (as caspase activators and caspase



1	276	100.0	276	14	US-10-032-159A-17	Sequence 17, Appl
2	276	100.0	417	14	US-10-032-159A-15	Sequence 15, Appl
3	276	100.0	3012	9	US-09-767-215-3	Sequence 3, Appl
4	276	100.0	3417	9	US-09-767-215-4	Sequence 4, Appl
5	276	100.0	3766	12	US-10-04-047-315	Sequence 315, App
6	276	100.0	3931	9	US-09-767-215-1	Sequence 1, Appl
7	113.4	41.1	3096	11	US-09-798-412-9	Sequence 9, Appl
8	113.4	41.1	3096	11	US-10-325-917-9	Sequence 9, Appl
9	113.4	41.1	3949	11	US-09-798-412-7	Sequence 7, Appl
10	113.4	41.1	3949	15	US-10-325-917-7	Sequence 7, Appl
11	100.4	36.4	276	14	US-10-032-159A-9	Sequence 9, Appl
12	100.4	36.4	3441	11	US-09-798-412-12	Sequence 12, Appl
13	100.4	36.4	3441	15	US-10-325-917-12	Sequence 12, Appl
14	100.4	36.4	3744	14	US-10-032-159A-7	Sequence 7, Appl
15	100.4	36.4	4276	11	US-09-798-412-10	Sequence 10, Appl

16	100.4	36.4	4276	15	US-10-325-917-10	Sequence 10, Appl
17	92.6	33.6	514	10	US-09-796-699-3360	Sequence 3560, Appl
18	92.6	33.6	514	12	US-10-057-475B-3560	Sequence 3560, Appl
19	92.6	33.6	514	15	US-10-154-884B-3560	Sequence 3560, Appl
20	92.6	33.6	514	15	US-10-040-868B-3560	Sequence 3560, Appl
21	88	31.9	1101	11	US-09-732-159A-1	Sequence 1, Appl
22	88	31.9	1608	11	US-09-798-412-6	Sequence 6, Appl
23	88	31.9	1608	15	US-10-325-917-6	Sequence 6, Appl
24	88	31.9	2098	15	US-09-798-412-4	Sequence 4, Appl
25	88	31.9	2098	15	US-10-325-917-4	Sequence 4, Appl
26	88	31.9	2176	14	US-10-032-159A-19	Sequence 19, Appl
27	79.6	28.8	1608	11	US-09-798-412-3	Sequence 3, Appl
28	79.6	28.8	1608	15	US-10-325-917-3	Sequence 3, Appl
29	79.6	28.8	1879	15	US-09-798-417-1	Sequence 1, Appl
30	79.6	28.8	1879	15	US-10-325-917-1	Sequence 1, Appl
31	69.8	25.3	216	14	US-10-032-159A-3	Sequence 3, Appl
32	66.8	24.2	1141	14	US-10-032-159A-37	Sequence 37, Appl
33	50.2	18.2	281	14	US-10-032-159A-21	Sequence 21, Appl
34	49	17.8	858	14	US-10-027-632-166977	Sequence 166977, Appl
35	49	17.8	858	14	US-10-027-632-166977	Sequence 166977, Appl
36	48.2	17.5	804	13	US-10-027-632-172688	Sequence 172688, Appl
37	48.2	17.5	804	14	US-10-027-632-172688	Sequence 172688, Appl
38	47.8	17.3	500	13	US-10-029-386-12805	Sequence 12805, Appl
39	44.4	16.1	145	13	US-10-029-386-26505	Sequence 26505, Appl
40	44.4	16.0	1230	12	US-10-369-493-42937	Sequence 42937, Appl
41	43.6	15.8	1140	12	US-10-369-493-41640	Sequence 41640, Appl
42	42.8	15.5	1365	12	US-10-369-493-32426	Sequence 32426, Appl
43	42.8	15.5	1548	12	US-10-369-493-31289	Sequence 31289, Appl
44	42.8	15.5	2121	12	US-10-369-493-28530	Sequence 28530, Appl
45	42	15.2	569	13	US-10-029-386-2514	Sequence 2514, Appl

## ALIGNMENTS

RESULT 1  
US-10-032-159A-17

Publication No. US20020164703A1

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Godzik, Adam

10 TITLE OF INVENTION: ENCODING NUCLEIC ACIDS, AND METHOD  
11 THEREOF. D 17 5100

CURRENT APPLICATION NUMBER: US/10/032,159A  
CURRENT FILING DATE: 2001-12-19

PRIOR FILING DATE: 2000-12-21

```

1 NUMBER OF SEQ ID NOS: 57
2 SOFTWARE: FastSeq for Windows Version 4.0.0
3

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LENGTH: 2

**ORGANISM:** Homo sapiens

NAME/KEY: CDS

US-10-032-159A-1

Query Match	100.0%;	Score 2/6;	DB 14;	Length 2/6;
Best Local Similarity	100.0%;	Prod NO 7	1e-66;	

DATE	TIME	LOCATION	WIND DIRECTION	WIND SPEED	SEA STATE	WEATHER	REMARKS
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1968-07-10	1200	OFF SHORE	090	10 KNOTS	3	B, C	
1968-07-10	1600	OFF SHORE	090	10 KNOTS	3	B, C	
1968-07-10	2000	OFF SHORE	090	10 KNOTS	3	B, C	
1968-07-11	0800	OFF SHORE	090	10 KNOTS	3	B, C	
1968-07-11	1200	OFF SHORE	090	10 KNOTS	3	B, C	
1968-07-11	1600	OFF SHORE	090	10 KNOTS	3	B, C	
1968-07-11	2000	OFF SHORE	090	10 KNOTS	3	B, C	

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

61 CCCAGCCGCTCACCCCTACCTGCGCCAGGCCAAGTGCTGTGCCAGCTGGACGAG 120

DB 61 CCCAGCCGCTCACCCCTACCTGCGCCAGGCCAAGTGTGTGCGCAGCTGGACGAGAG 120

QY 121 GAGGTGCTGACAGCCCGGCTCAACCAAGCCGATCGGGCCGGCACTTGTGAT 180  
DB 121 GAGGTGCTGACAGCCCGGCTCAACCAAGCCGATCGGGCCGGCACTTGTGAT 180  
QY 181 TTGCTGAAGACTGAGGGAAGAAACGGGGCCATCGCTTCTTGAAGAGCTGAAGTTCCAC 240  
DB 181 TTGCTGAAGACTGAGGGAAGAAACGGGGCCATCGCTTCTTGAAGAGCTGAAGTTCCAC 240  
QY 241 AACCTGAGCTGACACCTGATCAACCGGGCTGACAG 276  
DB 241 AACCTGAGCTGACACCTGATCAACCGGGCTGACAG 276

RESULT 2  
US-10-032-159a-15

Sequence 15, Application US/10032159A  
Publication No. US20020164703A1  
GENERAL INFORMATION:  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,  
FILE REFERENCE: P-LJ 5100  
CURRENT APPLICATION NUMBER: US/10/032,159A  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: US 60/257,457  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 417  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(417)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 416, 417  
OTHER INFORMATION: n = A,T,C or G  
US-10-032-159a-15

Query Match 100.0%; Score 276; DB 14; Length 417;  
Best Local Similarity 100.0%; Pred.No. 7,2e-66;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGGAGATGATGAGAGCCACCGCCACAGATGTGACGTGCTGTC 60  
DB 46 GAGGAGACACTGTGGGAGATGATGAGAGCCACCGCCACAGATGTGACGTGCTGTC 105  
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DB 106 CCCAGCGGCTCAACCCCTACCTGGGCGAGGCCAAGGTCGTGACAGTGAAGAGAG 165  
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DB 166 GAGGTGCTGACAGCCCGGCTCAACCAAGCCGATCGGGCCGGCACTTGTGAT 225  
QY 181 TTGCTGAAGACTGAGGGAAGAAACGGGGCCATCGCTTCTTGAAGAGCTGAAGTTCCAC 240  
DB 226 TTGCTGAAGACTGAGGGAAGAAACGGGGCCATCGCTTCTTGAAGAGCTGAAGTTCCAC 285  
QY 241 AACCTGAGCTGACACCTGATCAACCGGGCTGACAG 276  
DB 286 AACCTGAGCTGACACCTGATCAACCGGGCTGACAG 321

RESULT 3  
US-09-767-215-3  
Sequence 3, Application US/09767215  
Patent No. US2002081636A1  
GENERAL INFORMATION:

APPLICANT: Berlin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 07334-142001  
CURRENT APPLICATION NUMBER: US/09/767,215  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: 60/181,159  
PRIOR FILING DATE: 2000-02-09  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 3012  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-767-215-3

Query Match 100.0%; Score 276; DB 9; Length 3012;  
Best Local Similarity 100.0%; Pred.No. 7,6e-66;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGGAGATGATGAGAGCCACCGCCACAGATGTGACGTGCTGTC 60  
DB 46 GAGGAGACACTGTGGGAGATGATGAGAGCCACCGCCACAGATGTGACGTGCTGTC 105  
QY 61 CCCAGCGGCTCAACCCCTACCTGGGCGAGGCCAAGGTCGTGACAGTGAAGAGAG 120  
DB 106 CCCAGCGGCTCAACCCCTACCTGGGCGAGGCCAAGGTCGTGACAGTGAAGAGAG 165  
QY 121 GAGGTGCTGACAGCCCGGCTCAACCAAGCCGATCGGGCCGGCACTTGTGAT 180  
DB 166 GAGGTGCTGACAGCCCGGCTCAACCAAGCCGATCGGGCCGGCACTTGTGAT 225  
QY 181 TTGCTGAAGACTGAGGGAAGAAACGGGGCCATCGCTTCTTGAAGAGCTGAAGTTCCAC 240  
DB 226 TTGCTGAAGACTGAGGGAAGAAACGGGGCCATCGCTTCTTGAAGAGCTGAAGTTCCAC 285  
QY 241 AACCTGAGCTGACACCTGATCAACCGGGCTGACAG 276  
DB 286 AACCTGAGCTGACACCTGATCAACCGGGCTGACAG 321

RESULT 4  
US-09-767-215-4  
Sequence 4, Application US/09767215  
Patent No. US2002081636A1  
GENERAL INFORMATION:

APPLICANT: Berlin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 07334-142001  
CURRENT APPLICATION NUMBER: US/09/767,215  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: 60/181,159  
PRIOR FILING DATE: 2000-02-09  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 3417  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(3417)  
US-09-767-215-4

Query Match 100.0%; Score 276; DB 9; Length 3417;  
Best Local Similarity 100.0%; Pred.No. 7,6e-66;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGGAGATGATGAGAGCCACCGCCACAGATGTGACGTGCTGTC 60  
DB 46 GAGGAGACACTGTGGGAGATGATGAGAGCCACCGCCACAGATGTGACGTGCTGTC 105

QY 61 CCCAGCCGCTCTACCCCTTACTGCGCCAGGCGCAAGTGTCTGTGCGACGTGACGAGAG 120  
DB 106 CCCAGCCGCTCTACCCCTTACTGCGCCAGGCGCAAGTGTCTGTGCGACGTGACGAGAG 165  
QY 121 GAGGTGCTGACAGAGCCCGGCTGACCAAGAGCGCATGCGGAGCCGGGCACTGTGAGAT 180  
DB 166 GAGGTGCTGACAGAGCCCGGCTGACCAAGAGCGCATGCGGAGCCGGGCACTGTGAGAT 225  
QY 181 TTGCTGAAGACTCGAGGGAAGAACGGGGCATGCGCTTCTGTGAGAGCTGAAGTTCCAC 240  
DB 226 TTGCTGAAGACTCGAGGGAAGAACGGGGCATGCGCTTCTGTGAGAGCTGAAGTTCCAC 285  
QY 241 AACCTGACGTCTACACCTTGTCAACCGGCTGACG 276  
DB 286 AACCTGACGTCTACACCTTGTCAACCGGCTGACG 321

RESULT 5  
US-10-104-047-315  
; Sequence 315, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HEMIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patentn Ver. 2.1  
; SEQ ID NO 315:  
; LENGTH: 3766  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-315

Query Match 100.0%; Score 276; DB 12; Length 3766;  
Best Local Similarity 100.0%; Pred. No. 7.6e-66;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCACCGGCAAGATGTACGCTGATCTGC 60  
DB 237 GAGGAGACACTGTGGAGATGATGAGAGCCACCGGCAAGATGTACGCTGATCTGC 296  
QY 61 CCCAGCCGCTCTACCCCTTACTGCGCCAGGCGCAAGTGTCTGTGCGACGTGACGAGAG 120  
DB 297 CCCAGCCGCTCTACCCCTTACTGCGCCAGGCGCAAGTGTCTGTGCGACGTGACGAGAG 356  
QY 121 GAGGTGCTGACAGAGCCCGGCTGACCAAGAGCGCATGCGGAGCCGGGCACTGTGAGAT 180  
DB 357 GAGGTGCTGACAGAGCCCGGCTGACCAAGAGCGCATGCGGAGCCGGGCACTGTGAGAT 416  
QY 181 TTGCTGAAGACTCGAGGGAAGAACGGGGCATGCGCTTCTGTGAGAGCTGAAGTTCCAC 240  
DB 417 TTGCTGAAGACTCGAGGGAAGAACGGGGCATGCGCTTCTGTGAGAGCTGAAGTTCCAC 476  
QY 241 AACCTGACGTCTACACCTTGTCAACCGGCTGACG 276  
DB 477 AACCTGACGTCTACACCTTGTCAACCGGCTGACG 512

RESULT 6  
US-09-767-215-1  
; Sequence 1, Application US/09767215  
; Patent No. US20020081636A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 0734-142001  
; CURRENT APPLICATION NUMBER: US/09/767,215  
; CURRENT FILING DATE: 2001-01-22

PRIOR APPLICATION NUMBER: 60/181,159  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (207)...(3218)  
US-09-767-215-1

Query Match 100.0%; Score 276; DB 9; Length 3931;  
Best Local Similarity 100.0%; Pred. No. 7.7e-66;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCACCGGCAAGATGTACGCTGATCTGC 60  
DB 252 GAGGAGACACTGTGGAGATGATGAGAGCCACCGGCAAGATGTACGCTGATCTGC 311  
QY 61 CCCAGCCGCTCTACCCCTTACTGCGCCAGGCGCAAGTGTCTGTGCGACGTGACGAGAG 120  
DB 312 CCCAGCCGCTCTACCCCTTACTGCGCCAGGCGCAAGTGTCTGTGCGACGTGACGAGAG 371  
QY 121 GAGGTGCTGACAGAGCCCGGCTGACCAAGAGCGCATGCGGAGCCGGGCACTGTGAGAT 180  
DB 372 GAGGTGCTGACAGAGCCCGGCTGACCAAGAGCGCATGCGGAGCCGGGCACTGTGAGAT 431  
QY 181 TTGCTGAAGACTCGAGGGAAGAACGGGGCATGCGCTTCTGTGAGAGCTGAAGTTCCAC 240  
DB 432 TTGCTGAAGACTCGAGGGAAGAACGGGGCATGCGCTTCTGTGAGAGCTGAAGTTCCAC 491  
QY 241 AACCTGACGTCTACACCTTGTCAACCGGCTGACG 276  
DB 492 AACCTGACGTCTACACCTTGTCAACCGGCTGACG 527

RESULT 7  
US-09-798-412-9  
; Sequence 9, Application US/09798412  
; Publication No. US20030109428A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 0734-327001  
; CURRENT APPLICATION NUMBER: US/09/798,412  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 09/728,260  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 09/685,791  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/513,904  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: US 09/507,533  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: US 60/168,780  
; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 3096  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-798-412-9

Query Match 41.1%; Score 113.4; DB 11; Length 3096;  
Best Local Similarity 63.3%; Pred. No. 1.5e-21;  
Matches 174; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCACCGGCAAGATGTACGCTGATCTGC 60

```
DB 70 GAGAGCGCGCTGTGGAGCGAATCGAGGGGCTCCGGCATGGCTGGCTGGCCCTTGAAAC 129
QY 61 CCCAGCGCGCTCAACCCCTTAACCTGCGCCAGGCGCAAGTGTGTGCCAGCTGACAGAGAG 120
DB 130 CCGGCGCAAGCTCAACCGCTGTCTGCGCCAGTGCCTGGGTATCATGACAGAGGAGCGAGAG 189
QY 121 GAGGTGCTGACAGCCCCCGGCTCACCAGACGCGCATGCGGGGCACTTGTCTGAT 180
DB 190 GAGGTGCTGACAGCTTACCGCTTCCGCTGCGCATGACGCGCCGCGGCTGATGAGAC 249
QY 181 TTGCTGAAGACTGAGGAGAGAAACGGGGCCATGCGCTTCTGAGAGCCTGAAGTTCCAC 240
DB 250 ATCTTGCGCTGCCGTGCGCAAGAGGGGCTATGAGGCTTCTGGAAGCCCTGAGTTCTAC 309
QY 241 AACCTGACGTCTACACCCCTGTCACCGGAGCTGCA 275
DB 310 TACCCGAAACACTTCAACGCTGCTCAACGGGCGCAGGA 344

RESULT 8
US-10-325-917-9
; Sequence 9, Application US/10325917
; Publication No. US20030113787A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-327001
; CURRENT APPLICATION NUMBER: US/10/325,917
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/09/798,412
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-917-9
```

```
Query Match 41.1%; Score 113.4; DB 15; Length 3096;
Best Local Similarity 63.3%; Pred. No. 1.5e-21;
Matches 174; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
```

```
QY 1 GAGAGACACTGTGGAGATGATGAGAGCCACCGCCACAGATCTGATCTGATCTGC 60
DB 70 GAGAGACGCGCTGTGGAGCGAATCGAGGGGCTCCGGCATGGCTGGCTGGCCCTTGAAAC 129
QY 61 CCCAGCGCGCTCAACCCCTTAACCTGCGCCAGGCGCAAGTGTGTGCCAGCTGACAGAGAG 120
DB 130 CCGGCGCAAGCTCAACCGCTGTCTGCGCCAGTGCCTGGGTATCATGACAGAGGAGCGAGAG 189
QY 121 GAGGTGCTGACAGCCCCCGGCTCACCAGACGCGCATGCGGGGCACTTGTCTGAT 180
DB 190 GAGGTGCTGACAGCTTACCGCTTCCGCTGCGCATGACGCGCCGCGGCTGATGAGAC 249
QY 181 TTGCTGAAGACTGAGGAGAGAAACGGGGCCATGCGCTTCTGAGAGCCTGAAGTTCCAC 240
DB 250 ATCTTGCGCTGCCGTGCGCAAGAGGGGCTATGAGGCTTCTGGAAGCCCTGAGTTCTAC 309
QY 241 AACCTGACGTCTACACCCCTGTCACCGGAGCTGCA 275
DB 310 TACCCGAAACACTTCAACGCTGCTCAACGGGCGCAGGA 344
```

```
RESULT 9
US-09-798-412-7
; Sequence 7, Application US/09798412
; Publication No. US20030109428A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-327001
; CURRENT APPLICATION NUMBER: US/09/798,412
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/685,791
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/513,904
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/507,533
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/168,780
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3949
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)...(3136)
US-09-798-412-7
```

```
Query Match 41.1%; Score 113.4; DB 11; Length 3949;
Best Local Similarity 63.3%; Pred. No. 1.6e-21;
Matches 174; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
```

```
QY 1 GAGAGACACTGTGGAGATGATGAGAGCCACCGCCACAGATCTGATCTGATCTGC 60
DB 110 GAGAGACGCGCTGTGGAGCGAATCGAGGGGCTCCGGCATGGCTGGCTGGCCCTTGAAAC 169
QY 61 CCCAGCGCGCTCAACCCCTTAACCTGCGCCAGGCGCAAGTGTGTGCCAGCTGACAGAGAG 120
DB 170 CCGGCGCAAGCTCAACCGCTGTCTGCGCCAGTGCCTGGGTATCATGACAGAGGAGCGAGAG 229
QY 121 GAGGTGCTGACAGCCCCCGGCTCACCAGACGCGCATGCGGGGCACTTGTCTGAT 180
DB 230 GAGGTGCTGACAGCTTACCGCTTCCGCTGCGCATGACGCGCCGCGGCTGATGAGAC 289
QY 181 TTGCTGAAGACTGAGGAGAGAAACGGGGCCATGCGCTTCTGAGAGCCTGAAGTTCCAC 240
DB 290 ATCTTGCGCTGCCGTGCGCAAGAGGGGCTATGAGGCTTCTGGAAGCCCTGAGTTCTAC 349
QY 241 AACCTGACGTCTACACCCCTGTCACCGGAGCTGCA 275
DB 350 TACCCGAAACACTTCAACGCTGCTCAACGGGCGCAGGA 384

RESULT 10
US-10-325-917-7
; Sequence 7, Application US/10325917
; Publication No. US20030113787A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-327001
; CURRENT APPLICATION NUMBER: US/10/325,917
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/09/798,412
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/728,260
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Db 274 TACCCAGAACTGTACAACTGTGACTGG 303

## RESULT 13

US-10-325-917-12  
; Sequence 12, Application US/10325917  
; Publication No. US20030113787A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-327001  
; CURRENT APPLICATION NUMBER: US/10/325,917  
; PRIOR FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US/09/798,412  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 09/728,260  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 09/685,791  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/513,904  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: US 09/507,533  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: US 60/168,780  
; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 3441  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-325-917-12

Query Match 36.4%; Score 100.4; DB 15; Length 3441;  
Best Local Similarity 60.7%; Pred. No. 5,4e-18;  
Matches 164; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCACCGCCACAGATCTGATCTGCTGCG 60  
DB 34 GAGGAGCCCTTGTGGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 93  
QY 61 CCAGCCGCTCAACCCCTCACTGCGCCAGGCGCAAGGCTGCTGAGGAGGAG 120  
DB 94 CCGCCAGGCTCAAGGCGCTCACTGCGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 153  
QY 121 GAGGCTGTCAGACGCGCGCTCAACCAACAGCGCCATCGGCGCGCTGCTGAT 180  
DB 154 GAGGCTTATATCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213  
QY 181 TTGCTGAAGCTCAGAGGAAAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 214 ATTCTACATCAAGGCGGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273  
QY 241 AACCTGAGCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270  
DB 274 TACCCAGAACTGTACAACTGTGACTGG 303

## RESULT 14

US-10-032-159a-7  
; Sequence 7, Application US/10032159A  
; Publication No. US20020164703A1  
; GENERAL INFORMATION:  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,  
; FILE REFERENCE: P-1J 5100.  
; CURRENT APPLICATION NUMBER: US/10/032,159A  
; CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US 60/257,457  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3744  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ... (3744)  
US-10-032-159a-7

Query Match 36.4%; Score 100.4; DB 14; Length 3744;  
Best Local Similarity 60.7%; Pred. No. 5,4e-18;  
Matches 164; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCACCGCCACAGATCTGATCTGCTGCG 60  
DB 34 GAGGAGCCCTTGTGGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 93  
QY 61 CCAGCCGCTCAACCCCTCACTGCGCCAGGCGCAAGGCTGCTGAGGAGGAGGAG 120  
DB 94 CCGCCAGGCTCAAGGCGCTCACTGCGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 153  
QY 121 GAGGCTGTCAGACGCGCGCTCAACCAACAGCGCCATCGGCGCGCTGCTGAT 180  
DB 154 GAGGCTTATATCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213  
QY 181 TTGCTGAAGCTCAGAGGAAAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 214 ATTCTACATCAAGGCGGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273  
QY 241 AACCTGAGCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270  
DB 274 TACCCAGAACTGTACAACTGTGACTGG 303

## RESULT 15

US-09-798-412-10  
; Sequence 10, Application US/09798412  
; Publication No. US20030109428A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-327001  
; CURRENT APPLICATION NUMBER: US/09/798,412  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: US 09/728,260  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 09/685,791  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/513,904  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: US 09/507,533  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: US 60/168,780  
; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 4276  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (328) ... (3768)  
US-09-798-412-10

Query Match 36.4%; Score 100.4; DB 11; Length 4276;  
Best Local Similarity 60.7%; Pred. No. 5,4e-18;  
Matches 164; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
QY      1 GAGGAGCACTGTGGGAGATGATGAGAGCCACCGCCACAGATCGATCGCTGATCTGC 60
Db      361 GAGGAGCGCTTGTGGGAGATGTGAGTGTATACCGGCACATGCTCAGCGCTATATCAAC 420
QY      61 CCCAGCGGCTCAACCCCTTACTGCGCCAGGCCAAGGTGCTGTGCCAGCTGACGAGAG 120
Db      421 CTTGCCAAGCTCAGCGCTTACTGCGCTCAATGTAAAGTCAITGATGAGCAGATGAAGAT 480
QY      121 GAGGTGCTGACAGCGCCCGGCTCACCAACAGCGCCATGCGGCGCGGCACTTGCTGAT 180
Db      481 GAAGTGCTTATGCGCCCTATGCTGCATCCAGATCAACGAGCAGGCGGCTGTGGAC 540
QY      181 TTGCTGAAGACTCGAGGGAAGAACGGGCGCATGCGCTTCTTGAAGAGCTGAAGTTCCAC 240
Db      541 ATTCTACATACCAAGGGGCAAAAGGGGCTATGTGTCTTCTTGGAGAGCCTAAGATTAT 600
QY      241 AACCTGACGCTTACACCTGCTGACCGGG 270
Db      601 TACCGAGACTGTACAAACTGTGTGACTGG 630
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Search completed: February 10, 2004, 03:07:58  
Job time : 231 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 15:58:23 ; Search time 193 Seconds  
(without alignments)  
3860.336 Million cell updates/sec

Title: US-10-032-159A-17

Perfect score: 276  
Sequence: 1 gagagacacacgtgaggagat.....ccctgcaccggcgtcag 276

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: N\_Geneseq\_19Jun03.\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	100.0	417	25	ABX11431 Human caspase recr
2	276	100.0	3417	22	AAD13448 Human caspase recr
3	276	100.0	3931	22	AAD13447 Human caspase recr
4	113.4	41.1	3948	24	AAS98203 DNA encoding plako
5	113.4	41.1	3949	22	AAS05388 Human caspase recr
6	113.4	41.1	3949	24	ABA00333 Human CARD-10 CDNA
7	100.4	36.4	3744	25	ABX11430 Human caspase recr
8	100.4	36.4	4275	22	AAS05389 Human caspase recr

9	100.4	36.4	4276	24	ABA00334 Human CARD-11 CDNA
C 10	88	31.9	524	21	AACT5276 Human ORF831
C 11	88	31.9	524	24	ABN26534 Human ORF polynuc
12	88	31.9	765	22	AAH08620 Human CDNA clone (
13	88	31.9	2098	22	AAS05387 Human caspase recr
14	88	31.9	2098	24	ABA00332 Human CARD-9 CDNA
15	88	31.9	2176	22	AAH18321 Human CDNA sequenc
16	88	31.9	2176	25	ABX11432 DNA encoding caspa
17	79.6	28.8	1879	22	AAS05386 Rat caspase recr
18	79.6	28.8	1879	24	ABA00331 Rat CARD-9 CDNA
19	66.8	24.2	1141	25	ABX11449 Human CARD-12X exp
20	50.2	18.2	281	25	ABX11433 Human CARD-10X exp
21	43.4	15.7	5535	23	ABE03813 Drosophila melanog
22	42.2	15.3	10893	23	ABE03812 Drosophila melanog
23	42.2	15.3	2934	22	AAH10330 Human haematopoiet
24	41.8	15.1	2277	19	AAV13836 Homo sapiens mamma
25	41.8	15.1	2277	19	AAV05372 Human telomerase p
26	41.6	15.1	1562	24	ABG72815 Human MDR1 encodin
27	41.6	15.1	1779	22	AAH16344 Human sbgtrango79a
28	41.6	15.1	1779	24	ABG86161 Novel human gene
29	41.6	15.1	1811	24	ABK48387 DNA encoding novel
30	41.6	15.1	1860	24	ABK92037 Human CDNA encodin
31	41.6	15.1	2222	24	ABK62081 Human LP polypepti
32	41.6	15.1	2300	24	AAH41875 Human CGD CDNA 68
33	41.6	15.1	2338	25	ABG77432 Human CGD CDNA 68
34	41.2	14.9	309	24	ABJ74221 Corn tassal-deriva
C 35	41	14.9	1389	21	AAK63862 Human foetal liver
C 36	41	14.9	1545	21	AAK63861 Human foetal liver
C 37	41	14.9	2860	24	ABT06279 Human NOVA1 coding
38	41	14.9	2860	24	ABT06280 Human NOVA1 coding
39	41	14.9	3884	22	AAH21316 Human CDNA sequenc
40	41	14.9	3884	25	ACA04096 Human CDNA encodin
41	41	14.9	3884	25	ACA04095 Human CDNA encodin
42	41	14.9	3884	25	ABX89213 DNA encoding novel
43	40.6	14.7	981	24	ABQ39868 Oligonucleotide fo
C 44	40.6	14.7	981	24	ABQ39869 Oligonucleotide fo
45	40.6	14.7	1359	21	AA56705 Human transmembran

## ALIGNMENTS

RESULT 1	ABX11431	standard; CDNA; 417 BP.
ID	ABX11431	standard; CDNA; 417 BP.
XX	ABX11431	
AC	ABX11431	
XX	09-MAY-2003	(first entry)
XX	09-MAY-2003	(first entry)
DE	Human caspase recruitment domain containing protein, CARD-12X, CDNA.	
XX	CARD, caspase recruitment domain; apoptosis; cell adhesion; inflammation; cytokine receptor signalling; cancer; glioma; carcinoma; adenocarcinoma; CARD-containing polypeptide associated disorder; sarcoma; melanoma; ss; hamartoma; leukemia; lymphoma; keratinocyte hyperplasia; neoplasia; keloid; benign prostatic hypertrophy; inflammatory hyperplasia; fibrosis; reterositis; allergy; arthritis; lupus; Sjogren's syndrome; sepsis; gene; Crohn's disease; ulcerative colitis; graft versus host disease; stroke; abnormal cell death disease; myocardial infarction; heart failure; human; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV; CARD-12X; caspase activator; caspase inhibitor.	
XX	OS	Homo sapiens.
XX	Key	Location/Qualifiers
XX	Key	1..417
XX	CDS	/*tag= a
FT		/product= "CARD-12X"
FT		/partial
FT		/transl_except= (pos:415..417,aa:Xaa)
FT		/note= "No stop codon given. Xaa = unknown"
FT	misc_feature	46..321

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGACACTGTGGAGATGATGAGAGAGCCAGCCGACAGATGTCGCTGATCTGC 60  
 Db 252 GAGAGACACTGTGGAGATGATGAGAGAGCCAGCCGACAGATGTCGCTGATCTGC 311  
 QY 61 CCCAGCCGCTCAACCCCTTACCTGCGCCAGCCAGAGTCTGTCAGCTGAGCAGAG 120  
 Db 312 CCCAGCCGCTCAACCCCTTACCTGCGCCAGCCAGAGTCTGTCAGCTGAGCAGAG 371  
 QY 121 GAGGTCTGCAACAGCCCGGCTCAACCAACAGCGCCATGCGGCGCATCTGCTGAT 180  
 Db 372 GAGGTCTGCAACAGCCCGGCTCAACCAACAGCGCCATGCGGCGCATCTGCTGAT 431  
 QY 181 TTGCTGAAGACTGAGGAGAGAAACGGGGCATGCGCTTCTGGAAGCTGAAGTTCCAC 240  
 Db 432 TTGCTGAAGACTGAGGAGAGAAACGGGGCATGCGCTTCTGGAAGCTGAAGTTCCAC 491  
 QY 241 AACCTGACGTCTACACCCCTGCTCAACCGGCGCTGCAG 276  
 Db 492 AACCTGACGTCTACACCCCTGCTCAACCGGCGCTGCAG 527

## RESULT 4

AAS98203 standard; cDNA; 3948 BP.

AAS98203;

12-MAR-2002 (first entry)

DNA encoding plakoglobin interacting protein #3.

Human; plakoglobin; cytoskeletal; osteopathic; dermatological; cardiac;  
 plakoglobin related disease; skin carcinoma; acantholytic disease;  
 basal cell carcinoma; squamous cell carcinoma; Naxos disease; PCR primer;  
 extramammary Paget's disease; heart disease; skin blistering;  
 subcorneal acantholysis; Grover's disease; Halley-Halley's disease;  
 Darier's disease; ectodermal dysplasia; skin fragility syndrome; ss.

Homo sapiens.

WO200185933-A2.

15-NOV-2001.

02-MAY-2001; 2001WO-EP04872.

09-MAY-2000; 2000EP-0201668.

(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

Van Roy F, Bonne S, Vanlandschoot A;

WPI; 2002-062246/08.

P-PSDB; AAU73247.

New polypeptide, useful for treating skin carcinoma or acantholytic  
 disease such as Grover's and Darier's disease, comprises a protein  
 interacting with human plakoglobin and involved in transduction of  
 plakoglobin related signal to nucleus -

Claim 7; Figure 3; 98pp; English.

The invention relates to an isolated plakoglobin interacting polypeptide  
 (I). (I) is useful as a medicament and in the manufacture of a  
 medicament for treating plakoglobin related diseases, such as skin  
 carcinoma or an acantholytic disease, and to screen compounds that  
 interfere with the interaction of the polypeptide with plakoglobin  
 The plakoglobin related diseases include basal cell carcinoma, squamous  
 cell carcinoma, extramammary Paget's disease, Naxos disease, heart  
 diseases, skin blistering and acantholytic diseases such as subcorneal  
 acantholysis, Grover's disease, Halley-Halley's disease or Darier's

CC disease, and ectodermal dysplasia/skin fragility syndrome. AAS98201-  
 CC AAS98288 represent novel human plakoglobin interacting protein  
 CC coding sequences and PCR primers of the invention.  
 SO Sequence 3948 BP; 717 A; 1218 C; 1327 G; 686 T; 0 other;

Query Match 41.1%; Score 113.4; DB 24; Length 3948;  
 Best Local Similarity 63.3%; Pred. No. 1.6e-15;  
 Matches 174; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 GAGAGACACTGTGGAGATGATGAGAGAGCCAGCCGACAGATGTCGCTGATCTGC 60  
 Db 114 GAGAGACAGCTGTGGAGAGAAACGGGGCATGCGCTTCTGGAAGCTGAAGTTCCAC 173  
 QY 61 CCCAGCCGCTCAACCCCTTACCTGCGCCAGCCAGAGTCTGTCAGCTGAGCAGAG 120  
 Db 174 CCCAGCCGCTCAACCCCTTACCTGCGCCAGCCAGAGTCTGTCAGCTGAGCAGAG 233  
 QY 121 GAGGTCTGCAACAGCCCGGCTCAACCAACAGCGCCATGCGGCGCATCTGCTGAT 180  
 Db 234 GAGGTCTGCAACAGCCCGGCTCAACCAACAGCGCCATGCGGCGCATCTGCTGAT 233  
 QY 181 TTGCTGAAGACTGAGGAGAGAAACGGGGCATGCGCTTCTGGAAGCTGAAGTTCCAC 240  
 Db 294 ATCTGGCGCTGCGGTGCAAGAGGGGCTATGAGGCGCTTCTGGAAGCTGAAGTTCCAC 353  
 QY 241 AACCTGACGTCTACACCCCTGCTCAACCGGCGCTGCAG 275  
 Db 354 AACCTGACGTCTACACCCCTGCTCAACCGGCGCTGCAG 388

## RESULT 5

AAS05388 standard; cDNA; 3949 BP.

AAS05388;

12-SEP-2001 (first entry)

Human caspase recruitment domain, CARD-10 cDNA sequence.

Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB;  
 apoptosis; hyperproliferative disorder; autoimmune; neurological;  
 inflammatory disorder; viral infection; stress-related response; ss.

Homo sapiens.

Key Location/Qualifiers

CDs 41..3139

/tag= a

/product= "CARD-10"

/note= "ORF is specifically claimed"

WO200140468-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32716.

03-DEC-1999; 99US-0168780.

18-FEB-2000; 2000US-0507533.

25-FEB-2000; 2000US-0513904.

10-OCT-2000; 2000US-0685791.

(MILL-) WILLENITUM PHARM INC.

Bertin J;

WPI; 2001-367809/38.

P-PSDB; AAU01206.

Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10,  
 CARD-11, useful as targets for therapy, as immunogens, and in screening

PT and detection assays -

XX Claim 2; Fig 10A-10C; 145pp; English.

CC The present sequence encoding for novel human caspase recruitment  
 CC domain, CARD-10 is isolated from a human skin cDNA library.  
 CC Also described are novel human sequences for CARD-9 and CARD-11  
 CC (AAU01205, AAU01207) and rat CARD-9 (AAU01204). CARD-10 and  
 CC CARD-11 interact with Bcl-10 which is thought to activate nuclear factor  
 CC (NF)-kappaB and apoptosis. The sequences of the invention can be used for  
 CC treating a disorder associated with abnormal levels of apoptosis by  
 CC modulating the expression or activity of CARD-9, CARD-10, or CARD-11.  
 CC They can be used for the treatment of hyperproliferative disorders  
 CC (e.g. cancer), autoimmune disorders (e.g. systemic lupus erythematosus),  
 CC neurological disorders (e.g. Alzheimer's disease), inflammatory disorders  
 CC (e.g. Crohn's disease), and viral infection (e.g. HIV). The CARD  
 CC polypeptide, polynucleotide and an antibody which selectively binds to  
 CC CARD can be used in screening and detection assays (e.g. chromosomal  
 CC mapping, tissue typing), predictive medicine (prognostic assays,  
 CC monitoring clinical trials, and therapy (treatment and prophylaxis)). The  
 CC CARD polypeptide may be used to screen for drugs that bind to and/or  
 CC modulate it. CARD sequences are potential targets for regulating and  
 CC inflammation, cancer, NF-kappaB signaling, stress-related response and  
 CC apoptosis in human disease. A host cell containing a polynucleotide  
 CC encoding CARD can be used to create transgenic animals.

XX Sequence 3949 BP; 724 A; 1222 C; 1319 G; 684 T; 0 other;

SO Query Match 41.1%; Score 113.4; DB 22; Length 3949;

Best Local Similarity 63.3%; Pred. No. 1.6e-15;

Matches 174; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCAGCCGCAAGATCTGATCTGC 60

DB 110 GAGGACGGCTGTGGAGAGATGAGAGGCGCTCCGGCATCGGCTGGCCCTTAAAC 169

QY 61 CCCAGCGCCTCACCCCTACTGCGGCGCAAGGCGCTGTGCTCCAGTGGACGAGAG 120

DB 170 CCGGCGCAAGCTCAGCCCTATCTGTGGCCAGTCCGGGTATCGACGAGAGAGAGAG 229

QY 121 GAGGTGCTGACAGCCCGGCTCAACCAAGCCCAATGCGGCGCGGCACTTGTGAT 180

DB 230 GAGGTGCTGACAGCTTACCTGCTTCCGCGCTCAACGCAACCGGCGCTGATGAC 289

QY 181 TTGCTGAAGACTCGAGGAGAGAGAGCGGCGCATCGCTTCTGAGAGCCTGAAGTTCCAC 240

DB 290 ATCTGCGCTGCGGTGGAGAGAGGCGCTATGAGGCTTCTCGAAGCCTGAGATTCTAC 349

QY 241 AACCTGACGTCTACACCTTGTGACCGGGGCTGCA 275

DB 350 TACCCCGAACAATTACGCTGCTCACGGGCGCAGGA 384

RESULT 6

ABA00333

ID ABA00333 standard; cDNA; 3949 BP.

AC ABA00333;

DT 09-DEC-2002 (first entry)

DE Human CARD-10 cDNA.

XX Gene; rat; human; caspase recruitment domain; CARD-9; CARD-10;

XX CARD-11; apoptosis; inflammation; cell growth; cell death;

XX lymphocyte activation; cancer; melanoma; autoimmune disease;

XX arthritis; neurological disorder; Alzheimer's disease; ss.

OS Homo sapiens.

XX Key

FT CDS Location/Qualifiers

FT /product= "CARD-10"

PN MO200270652-A2.

PD 12-SEP-2002.

PF 28-FEB-2002; 2002MO-US06147.

PR 02-MAR-2001; 2001US-0798412.

PA (MILL-) MILLENNIUM PHARM INC.

PT Bertin J;

DR WPI; 2002-698749/75.

DR P-PDSB; AAG79554.

PT CARD-9, CARD-10 or CARD-11 polypeptides and polynucleotides, useful for

PT treating disorders associated with inappropriate apoptosis or

PS lymphocyte activation, e.g. cancer

XX Claim 5; Fig 10; 151pp; English.

XX This sequence encodes human caspase recruitment domain (CARD)-10.

XX CARD proteins play roles in apoptotic and inflammatory signalling

XX pathways. CARD-9, -10 and -11 participate in the network of

XX interactions that modulate caspase activity. They are thought to be

XX useful as modulating agents for regulating a variety of cellular

XX processes including cell growth and cell death. CARD proteins and

XX nucleic acids are useful for treating a disorder associated with

XX inappropriate apoptosis or lymphocyte activation or for diagnosing

XX subjects having or that are at risk of developing a disorder associated

XX with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such

XX as cancer e.g. melanoma, autoimmune disorders e.g. arthritis, or

XX neurological disorders e.g. Alzheimer's disease.

SO Sequence 3949 BP; 724 A; 1222 C; 1319 G; 684 T; 0 other;

Query Match 41.1%; Score 113.4; DB 24; Length 3949;

Best Local Similarity 63.3%; Pred. No. 1.6e-15;

Matches 174; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 GAGGAGACACTGTGGAGATGATGAGAGCCAGCCGCAAGATCTGATCTGC 60

DB 110 GAGGAGCGCTGTGGAGAGATGAGAGGCGTCCGCAATGCGCTGCGCCCTGAAC 169

QY 61 CCCAGCGCCTCAACCCCTACTGCGCGCAGGCGCAAGTGTGCGAGCTGAGAGAGAG 120

DB 170 CCGGCGCAAGCTCAGCCCTATCTGTGGCCAGTCCGGGTATCGACGAGAGAGAGAG 229

QY 181 TTGCTGAAGACTCGAGGAGAGAGAGCGGCGCATCGCTTCTGAGAGCCTGAAGTTCCAC 240

DB 290 ATCTGCGCTGCGGTGGAGAGAGGCGCTATGAGGCTTCTCGAAGCCTGAGATTCTAC 349

QY 241 AACCTGACGTCTACACCTTGTGACCGGGGCTGCA 275

DB 350 TACCCCGAACAATTACGCTGCTCACGGGCGCAGGA 384

RESULT 7

ABX11430

ID ABX11430 standard; cDNA; 3744 BP.

AC ABX11430;

DT 09-MAY-2003 (first entry)

DE Human caspase recruitment domain containing protein, CARD-11X, cDNA.

Query Match	Score	DB	Length
36.4%	Score 100.4	DB 25	Length 3744

Matches	154;	Conservative	0;	Mismatches	106;	Indels	0;	Gaps	0;
QY	1	GAGGAGACACTGTGGAGATGATGAGAGACCAACCGCCACAGATCGTACGCTGATCTGCG	60						
Db	34	GAGGAGCGCTTGTGGAGATGATGAGATGTAAACCGGACATGCTCAACCGCTATATCAAC	93						
QY	61	CCGACGCGGCTCACCCCTACCTCGCGGACGCGCAAGGTGTGCGCCAGCTGACGAGAG	120						
Db	94	CTGCGCAAGCTCACCGCTACCTCGCTGAGTAAAGTCAATGATAGGACGATGAAGAT	153						
QY	121	GAGGTCTGCAAGCGCCCGGCTACCAACAGCGCCATGCGGCGCGGACATTGCTGAT	180						
Db	154	GAAAGTCTTAAAGCCCTATGCTGCATCCAAGTCAACCGACGACCGCGCTGTGGAC	213						
QY	181	TTCCTGAAGACTCGAGGAGAGAACGGGGCCATGCGCTTCTGTGAGAGCTGAAGTTCCAC	240						
Db	214	ATTCTACATACCAAGGGGCAAAGGGGCTAATGTGATCTTTTGGAGAGCTGAAATTTAT	273						
QY	241	AACCTGAAGTCTACACCTCTGTCAACCGGG	270						
Db	274	TACCCAGACTGTACAACTGTGTACTGGG	303						
RESULT 8									
AA505389	standard; cDNA; 4275 BP.								
AA505389	standard; cDNA; 4275 BP.								
AA505389	standard; cDNA; 4275 BP.								
DT	12-SEP-2001	(first entry)							
DE	Human caspase recruitment domain, CARD-11 cDNA sequence.								
XX	Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB; apoptosis; hyperproliferative disorder; autoimmune; neurological; inflammatory disorder; viral infection; stress-related response; ss.								
XX	Homo sapiens.								
XX	Key	Location/Qualifiers							
XX	CDS	327..3770							
XX	FT	/tag=a							
XX	FT	/product="CARD-11"							
XX	XX	/note="ORF is specifically claimed"							
XX	XX	MO200140468-A2.							
XX	07-JUN-2001.								
XX	01-DEC-2000; 2000WO-US32716.								
XX	03-DEC-1999; 99US-0168780.								
XX	18-FEB-2000; 2000US-0507533.								
XX	25-FEB-2000; 2000US-0513904.								
XX	10-OCT-2000; 2000US-0685791.								
XX	(MILL-) MILLENNIUM PHARM INC.								
XX	Bertin J.								
XX	WPI; 2001-367809/38.								
XX	P-PSDB; AAU01207.								
XX	Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-11, useful as targets for therapy, as immunogens, and in screening and detection assays -								
XX	Claim 2; Fig 14A-14C; 145pp; English.								
XX	The present sequence encoding for novel human caspase recruitment domain, CARD-11 is isolated from a human T-cell cDNA library. Also described are novel human sequences for CARD-9 and CARD-10								





neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 cholesterol ester storage; systemic lupus erythematosus; infection;  
 severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 thrombosis; contraceptive; ss.  
 Homo sapiens.  
 WO200058473-A2.  
 05-OCT-2000.  
 31-MAR-2000; 2000WO-US08621.  
 31-MAR-1999; 99US-0127607.  
 02-APR-1999; 99US-0127636.  
 05-APR-1999; 99US-0127728.  
 30-MAR-2000; 2000US-0540763.  
 (CURA-) CURAGEN CORP.  
 Shinkets RA, Leach M;  
 MPI; 2000-602362/57.  
 P-PSDB; AAB41067.  
 Novel nucleic acids and peptides derived from open reading frame X,  
 useful for treating e.g. cancers, proliferative disorders,  
 neurodegenerative disorders and cardiovascular disease -  
 Claim 5; Page 1326; 5507tp; English.

AACT74446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,  
 which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 sequences have activities such as: cytostatic; hepatotropic; vulnary;  
 antiproliferative; antiparkinsonian; neuroprotective;  
 osteoplastic; anticonvulsant; antiarthritic; immunosuppressant;  
 immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
 antidiabetic; hypotensive; dermatological; immunosuppressive;  
 antiinflammatory; antibacterial; antiviral; antifungal; antithrombotic;  
 antihypertensive; antianemic. The sequences can be used for determining  
 the presence of or predisposition to, or preventing or treating  
 pathological conditions associated with an ORFX-associated disorder. The  
 nucleic acids can be used to express ORFX proteins in gene therapy  
 vectors. The proteins and nucleic acids may be used to treat cancers,  
 proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 graft vs host disease, cardiovascular disease, diabetes mellitus,  
 hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 coagulation; to inhibit thrombosis; and as a contraceptive.

Sequence 524 BP; 87 A; 165 C; 171 G; 101 T; 0 other;

Query Match 31.9%; Score 89; DB 21; Length 524;  
 Best Local Similarity 58.3%; Pred. No. 4.1e-10;  
 Matches 154; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

13 TGGAGATGATGAGAGCCACCGCCACAGATGTAACGCTGATCTGCCCGCCGCGCTC 72  
 298 TGAAGCTCCTGGAGGGCTTCGGGCTGAGCGTCACTCCGATATCAACCCCTCAGGCATC 239  
 73 ACCCCCTACTGTCGCGACAGGCGCTGCTGCTGCACTGAGAGAGAGAGAGTGCAC 132  
 238 ACACCTTACTGTCGCGAGTGCAGAGGCTCTGAACCTGATGATGAGAGAGAGTGCAC 179  
 133 AGCCCCCGGCTACCAACAGCGCCATGCGGGCCGCGGACACTTGCTGATTTGCTGAAGCT 192  
 178 GACCCCACTGCTGATCCGCAACGAGAAAGTGGGTGTCTCTGATCACTCTCGACGCG 119

193 CGAGGGAAGAGAGGGGCGCATGCGCTTCTCGAGAGAGCTGAAGTTCCACACCGCTGACCTC 252  
 118 ACCGGGCAACAGAGGCTACCTGCGCTTCTCGAGAGCTGAGCTTACTACCGGAGCTG 59  
 253 TACACCTGCTACCGGCGCTGCG 276  
 58 TACAGAGGTCAACAGGCAAGAG 35

RESULT 11  
 AEN26534/c  
 ID AEN26534 standard; cDNA; 524 BP.  
 AEN26534;  
 24-JUN-2002 (first entry)  
 Human ORFX polynucleotide sequence SEQ ID NO:21545.

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;  
 degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 hypertension; hypothyroidism; cholesterol ester storage disease;  
 immune deficiency; immune disorder; infectious disease;  
 autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 myasthenia gravis; gene; ss.

Homo sapiens.  
 WO200192523-A2.  
 06-DEC-2001.  
 29-MAY-2001; 2001WO-US10836.  
 30-MAY-2000; 2000US-206132P.  
 29-AUG-2000; 2000US-228716P.  
 (CURA-) CURAGEN CORP.  
 Shinkets RA, Leach MD;  
 MPI; 2002-106308/14.  
 P-PSDB; ABP10782.

Novel human polypeptides and polynucleotides useful for diagnosing,  
 preventing and treating cardiovascular disease, neurodegenerative,  
 hyperproliferative disorders and autoimmune disorders -  
 Disclosure; SEQ ID 21545; 1037tp; English.

The present invention describes substantially purified human proteins  
 (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 in the specification)). AEN15762 to AEN27252 encode the human ORFX  
 proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 treating or preventing a pathology associated with an ORFX-associated  
 disorder in humans, and in the manufacture of a medicament for treating a  
 syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 sequences can be used in gene therapy. ORFX sequences can be used in the  
 treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
 osteoarthritis, neurodegenerative disorders, disorders related to organ  
 transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 storage disease, various immune deficiencies and disorders, rheumatoid  
 diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 bone degenerative disorders, or periodontal disease, and for gut  
 protection or regeneration and treatment of lung or liver fibrosis,





QY 193 CGAGGAGAGACGGGCGCCATCGCTTCTGGAAGCCTGAAGTTCCACCAACCTGACGTC 252  
 Db 354 ACCGCGCCACAAAGGCTCTACGTCGCTTCCTCGAGAGCCTGAGGCTTACTACTACCGCAGCTG 413  
 QY 253 TACACCTCGTTCACCGGCGCTGCAG 276  
 Db 414 TACAAGAGGTTCACGCGCAAGAG 437

## RESULT 15

AAH18321

ID AAH18321 standard; cDNA; 2176 BP.

AC AAH18321;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:18327.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI, 2001-318749/34.

PS Claim 8; SEQ ID 18327; 2537TP + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

SQ Sequence 2176 BP; 464 A; 657 C; 734 G; 321 T; 0 other;

Query Match 31.9%; Score 86; DB 22; Length 2176;  
 Best Local Similarity 58.3%; Pred. No. 4.5e-10;  
 Matches 154; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 13 TGGGAGATGATGAGAGAGCCACCGCCACAGAGATCGCTGATGCTGCGCCGCGCTC 72  
 Db 177 TGGAACTGCTGAGAGGCTTCGCGGTGAGCTCACTCGGTGATGACCCCTCAAGCATC 236  
 QY 73 ACCCCCTACCTGCGCCAGGCAAGGTGCTGTCAGCTGGAAGAAGAGAGTGTGCAAC 132  
 Db 237 ACACTTACTGCGGCAAGTGTGCTGGAAGCTTGAATGATGAGAGAGAGTGTGCAAC 296  
 QY 133 AGCCCCCGGCTCACCAAGAGCGCCATGCGGCGCGGCACTTGCTGATTTGCTGAAGACT 192  
 Db 297 GACCCCACTGCTGATCGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 356  
 QY 193 CGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 252  
 Db 357 ACCGCGCCACAAAGGCTACGTCGCTTCTCGAGAGCTGAGAGCTTACTACTACCGCAGCTG 416  
 QY 253 TACACCTCGTTCACCGGCGCTGCAG 276  
 Db 417 TACAAGAGGTTCACGCGCAAGAG 440

Search completed: February 10, 2004, 01:42:04  
 Job time : 198 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 9, 2004, 17:29:23 ; Search time 41 Seconds  
(without alignments)  
356.167 Million cell updates/sec

Title: US-10-032-159A-18  
Perfect score: 484  
Sequence: 1 EETLWEMSHRRHIVRCIC.....FLESLKFNPDYTLVTGLQ 92

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 5: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 6: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 7: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 8: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 9: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 10: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 11: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
- 12: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
- 13: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 14: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
- 15: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*
- 16: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*
- 17: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 18: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 19: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 20: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 21: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 22: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 23: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*
- 24: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	484	100.0	139	24 ABG76062 Human caspase recr
2	484	100.0	1004	22 AAE07164 Human caspase recr
3	484	100.0	1139	22 AAE07165 Human predicted ca
4	257	53.1	1147	22 AAU01207 Human caspase recr
5	257	53.1	1147	23 AAG79555 Human CARD-11. Ho
6	257	53.1	1247	24 ABG76061 Human caspase recr
7	237	49.0	1032	22 AAU01206 Human caspase recr
8	237	49.0	1032	23 AAG79554 Human CARD-10. Ho
9	237	49.0	1032	23 AAU73247 Human plakoglobin

10	207	42.8	536	22	AAU01204	Rat caspase recruit
11	207	42.8	536	23	AAG79552	Rat CARD-9. Rattu
12	199	41.1	174	21	AA041067	Human ORFX ORF831
13	199	41.1	174	23	ABP10782	Human ORFX protein
14	199	41.1	366	22	ABP95617	Human protein sequ
15	199	41.1	366	24	ABG76060	Caspase recruitment
16	199	41.1	536	22	AAU01205	Human caspase recr
17	199	41.1	536	23	AAG79553	Human CARD-9. Hom
18	93	19.2	237	23	AAU73245	Human plakoglobin
19	77	15.9	237	21	AA159412	Human CIPER protei
20	74	15.3	233	21	AA159413	Mouse CIPER protei
21	70	14.5	845	22	ABP62651	Drosophila melanog
22	69	14.3	1416	22	AAU30862	Novel human secret
23	68.5	14.2	497	23	ABP88899	Zinc finger protei
24	68	14.0	385	22	AA093386	Human polypeptide,
25	68	14.0	468	23	ABG7352	Human GED3, INCT
26	67.5	13.9	2443	22	ABP60521	Drosophila melanog
27	65.5	13.5	409	19	AAW76064	Ankyrin protein fr
28	65.5	13.5	409	19	AAW76772	D. immitis ankyrin
29	65.5	13.5	409	21	AA011585	D. immitis ankyrin
30	65.5	13.5	409	23	AA021364	Ankyrin protein se
31	65.5	13.5	422	23	AA021396	Ankyrin protein se
32	65.5	13.5	422	23	AA021396	Ankyrin protein se
33	65.5	13.5	1745	19	AAW76068	Full length ankyri
34	65.5	13.5	1745	19	AAW76776	D. immitis ankyrin
35	65.5	13.5	1745	21	AA011589	D. immitis ankyrin
36	65.5	13.5	1745	23	AA021368	Ankyrin protein se
37	65	13.4	639	22	ABP65465	Drosophila melanog
38	65	13.4	669	22	ABP77378	Rice acyl CoA oxid
39	65	13.4	676	22	ABP59664	Drosophila melanog
40	65	13.4	676	22	ABP66818	CtBP1-OVA-DD fusion
41	65	13.4	1266	22	AAE22544	Breast cancer asso
42	64	13.2	221	24	ABR47523	Human polypeptide,
43	64	13.2	412	22	AA093214	Human ORF897 prote
44	63.5	13.1	71	23	ABP31924	Human DITRP intrac
45	63.5	13.1	454	24	ABR41293	Human DITRP intrac

## ALIGNMENTS

RESULT 1  
ABG76062  
ID ABG76062 standard; protein; 139 AA.

09-MAY-2003 (first entry)

Human caspase recruitment domain containing protein, CARD-12X.

CARD, caspase recruitment domain; apoptosis; cell adhesion; inflammation;  
cytokine receptor signalling; cancer; glioma; carcinoma; adenocarcinoma;  
CARD-containing polypeptide associated disorder; sarcoma; melanoma;  
hamartoma; leukaemia; lymphoma; keratinocyte hyperplasia; neoplasia;  
keloid; benign prostatic hypertrophy; inflammatory hyperplasia; fibrosis;  
restenosis; allergy; arthritis; lupus; Sjogren's syndrome; sepsis; human;  
Crohn's disease; ulcerative colitis; graft versus host disease; stroke;  
abnormal cell death disease; myocardial infarction; heart failure;  
neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV;  
CARD-12X; caspase activator; caspase inhibitor.

Homo sapiens.

Key Location/Qualifiers  
FH 16..107  
FT /label= CARD  
FT /note= "Caspase recruitment domain. Specifically  
claimed in claim 12"

Misc-difference 139  
FT /label= Unknown  
FT /note= "Encoded by GNN"

XX	PN	US2002164703-A1.
XX	PD	07-NOV-2002.
XX	PF	19-DEC-2001; 2001US-0032159.
XX	PR	21-DEC-2000; 2000US-257457P.
XX	PA	(PAML/) PAWLOWSKI K.
XX	PA	(REED/) REED J C.
XX	PA	(GODZ/) GODZIK A.
XX	PI	Pawlowski K, Reed JC, Godzik A;
XX	DR	WPI; 2003-286137/28.
XX	DR	N-PSDB; ABX11431.
XX	PT	New isolated CARD-containing nucleic acids, useful for the diagnosis
XX	PT	and treatment of disorders with aberrant expression or activity of the
XX	PT	CARD-containing polypeptide, such as cancer, stroke, arthritis, heart
XX	PT	failure and AIDS
XX	PS	Claim 11; Fig 3; 34pp; English.
XX	CC	The invention relates to an isolated nucleic acid molecule encoding a
XX	CC	cardiac recruitment domain (CARD) containing polypeptide. CARD containing
XX	CC	polypeptides are involved in apoptosis (as caspase activators and caspase
XX	CC	inhibitors), cell adhesion, inflammation and cytokine receptor
XX	CC	signalling. The methods and compositions of the present invention are
XX	CC	useful for the diagnosis and treatment of disorders associated with the
XX	CC	aberrant expression or activity of the CARD containing polypeptide such
XX	CC	as cancer, glioma, carcinoma, adenocarcinoma, sarcoma, melanoma, keloid,
XX	CC	hamartoma, leukaemia, lymphoma, keratinocyte hyperplasia, neoplasia,
XX	CC	benign prostatic hypertrophy, inflammatory diseases such as arthritis, lupus,
XX	CC	restenosis, allergies, inflammatory diseases such as Crohn's disease,
XX	CC	Stogren's syndrome, Crohn's disease, ulcerative colitis, graft versus
XX	CC	host disease, sepsis, abnormal cell death diseases such as stroke,
XX	CC	myocardial infarction, heart failure, neurodegenerative diseases like
XX	CC	Parkinson's disease and Alzheimer's disease, and HIV infection. The
XX	CC	present sequence represents the amino acid sequence of the human
XX	CC	caspase recruitment domain containing protein, CARD-12X.
XX	SO	Sequence 139 AA;
QY		Query Match 100.0%; Score 484; DB 24; Length 139;
QY		Best Local Similarity 100.0%; Pred. No. 3.2e-57;
QY		Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY		1 EETLWEMESHRRIRYRCITPSRLTYLTAQAVYLCQDDEEFTLHSPRLTNSAPRAGHLD 60
DB		16 EETLWEMESHRRIRYRCITPSRLTYLTAQAVYLCQDDEEFTLHSPRLTNSAPRAGHLD 75
QY		61 LKTRGNKGAIAFLDSLKPENPVPVYTLVTLGQL 92
DB		76 LKTRGNKGAIAFLDSLKPENPVPVYTLVTLGQL 107
XX	RESULT 2	
XX	AAE07164	AAE07164 standard; Protein; 1004 AA.
XX	AAE07164;	
XX	DT	06-NOV-2001 (first entry)
XX	DE	Human caspase recruitment domain-14 (CARD-14).
XX	KX	Human; caspase recruitment domain-14; CARD-14; chromosome 17;
XX	KX	nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy;
XX	KX	autoimmune disorder; systemic lupus erythematosus; neurological disorder
XX	KX	Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia
XX	KX	haematological disorder; myelodysplastic syndrome; myocardial infarction
XX	KX	stroke; immune disorder; Crohn's disease; allergic rhinitis; infection;

KM	cell signalling disorder; cytostatic; immunosuppressive; nocotropic
KW	neuroprotective; antiviral; antibacterial.
XX	
OS	Homo sapiens.
FT	Key
FT	Modified-site
FT	Location/Qualifiers
FT	5..9
FT	/note= "GMP- and GMP-dependent protein kinase phosphorylation site"
FT	10..116
FT	/label= CARD_domain
FT	12..15
FT	"Casein kinase II phosphorylation site"
FT	18..21
FT	/note= "Casein kinase II phosphorylation site"
FT	25..27
FT	/note= "Protein kinase C phosphorylation site"
FT	60..62
FT	/note= "Protein kinase C phosphorylation site"
FT	91..93
FT	/note= "Protein kinase C phosphorylation site"
FT	114..117
FT	/note= "N-glycosylation site"
FT	117..122
FT	/note= "N-myristoylation site"
FT	121..123
FT	/note= "Protein kinase C phosphorylation site"
FT	126..420
FT	/label= Coiled_Coil_domain
FT	130..135
FT	/note= "N-myristoylation site"
FT	134..137
FT	/note= "Casein kinase II phosphorylation site"
FT	161..166
FT	/note= "N-myristoylation site"
FT	165..168
FT	/note= "Casein kinase II phosphorylation site"
FT	220..227
FT	/note= "Tyrosine kinase phosphorylation site"
FT	221..224
FT	/note= "Casein kinase II phosphorylation site"
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FT	/label= K-Box_domain
FT	240..243
FT	/note= "Casein kinase II phosphorylation site"
FT	250..252
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FT	253..256
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FT	259..262
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FT	307..309
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FT	307..310
FT	/note= "Casein kinase II phosphorylation site"
FT	359..365
FT	/note= "Tyrosine kinase phosphorylation site"
FT	366..368
FT	/note= "Protein kinase C phosphorylation site"
FT	366..369
FT	/note= "Casein kinase II phosphorylation site"
FT	378..381
FT	/note= "Casein kinase II phosphorylation site"
FT	384..386
FT	/note= "Protein kinase C phosphorylation site"
FT	385..406
FT	/note= "Leucine zipper pattern"

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FT Modified-site 463..465
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 470..472
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 501..504
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 511..516
FT /note= "N-myristoylation site"
FT Domain 568..660
FT /label= PDZ_domain
FT Modified-site 587..592
FT /note= "N-myristoylation site"
FT Modified-site 589..592
FT /note= "N-glycosylation site"
FT Modified-site 602..605
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FT Modified-site 634..637
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 653..655
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 674..677
FT /note= "Casein kinase II phosphorylation site"
FT Domain 676..745
FT /label= SH3_domain
FT Modified-site 714..719
FT /note= "N-myristoylation site"
FT Modified-site 725..727
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 725..728
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 733..738
FT /note= "N-myristoylation site"
FT Modified-site 737..740
FT /note= "N-glycosylation site"
FT Modified-site 759..761
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 760..763
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT Peptide 785..793
FT /note= "peroxisomal targeting signal"
FT Modified-site 796..799
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 800..805
FT /note= "N-myristoylation site"
FT Domain 826..1004
FT /label= Guanylate_kinase_domain
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FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 860..863
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 868..870
FT /note= "Protein kinase C phosphorylation site"
FT Region 870..872
FT /note= "RGD cell attachment sequence"
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FT /note= "Casein kinase II phosphorylation site"
FT Peptide 941..949
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FT Modified-site 976..979
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FT Modified-site 980..985
FT /note= "N-myristoylation site"
FT Modified-site 1003..1004
FT /note= "Protein kinase C phosphorylation site"

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XX
PN WO200159065-A2.
XX
PD 16-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US02087.
XX
PR 09-FEB-2000; 2000US-0181159.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Bertin J;
XX
DR WPI; 2001-497073/54.
XX
DR N-PSDB; AADI3447.
XX
PT An isolated caspase recruitment domain polypeptide useful for
PT regulating growth and cell death and useful for the treatment of cancer
PT
PS Claim 1; Fig 1A-1E; 109pp; English.
XX
PS The present sequence is human caspase recruitment domain-14 (CARD-14).
XX CC The CARD-14 gene is located on chromosome 17. The CARD-14 is used for
XX CC the detection of modulators that modulates the ability of CARD-14 to
XX CC bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation
XX CC of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulation
XX CC growth and cell death and useful for the treatment of cancer. It is
XX CC also useful for the treatment of autoimmune disorders (e.g., systemic
XX CC lupus erythematosus), neurological disorders (e.g., Alzheimer's and
XX CC Parkinson's disease, inflammatory disorders, hematological disorders
XX CC (e.g., anaemia, myelodysplastic syndromes), myocardial infarctions,
XX CC strokes, immune disorders (e.g., Crohn's disease, allergic rhinitis),
XX CC cell signalling disorders and certain viral and bacterial infections.
XX
SQ Sequence 1004 AA;
XX
Query Match 100.0%; Score 484; DB 22; Length 1004;
Best Local Similarity 100.0%; Pred. No. 4.9e-56;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EETLWEMESHRRIRVRCICPSRLTPYLRQAVLCQDDEEVLSHPRLTNSAMRAGHLID 60
DB 16 EETLWEMESHRRIRVRCICPSRLTPYLRQAVLCQDDEEVLSHPRLTNSAMRAGHLID 75
QY 61 LKTRGKGAIAFLBSLKFHPNDVYTLVGLQ 92
DB 76 LKTRGKGAIAFLBSLKFHPNDVYTLVGLQ 107
RESULT 3
AAE07165
ID AAE07165 standard; Protein; 1139 AA.
XX
AC AAE07165;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human predicted caspase recruitment domain-14 (CARD-14).
XX
DE Human; caspase recruitment domain-14; CARD-14; chromosome 17;
XX nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy;
XX autoimmune disorder; systemic lupus erythematosus; neurological disorder;
XX Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia;
XX haematological disorder; myelodysplastic syndrome; myocardial infarction;
XX stroke; immune disorder; Crohn's disease; allergic rhinitis; infection;
XX cell signalling disorder; cytostatic; immunosuppressive; neurotropic;
XX neuroprotective; antiviral; antibacterial.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 700

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FT	/note= "Encoded by TGS"
XX	WO200159065-A2.
XX	16-AUG-2001.
PD	22-JAN-2001; 2001WO-US02087.
XX	09-FEB-2000; 2000US-0181159.
XX	(MILL-) MILLENNIUM PHARM INC.
PA	Bertin J;
XX	WP1; 2001-497073/54.
DR	N-PSDB; AAD13448.
XX	An isolated caspase recruitment domain polypeptide useful for
PT	regulating growth and cell death and useful for the treatment of cancer
PT	-
PS	Disclosure; Fig 2A-2C; 109pp; English.
XX	The present sequence is predicted human caspase recruitment domain-14
CC	(CARD-14). The CARD-14 gene is located on chromosome 17. The CARD-14 is
CC	used for the detection of modulators that modulates the ability of
CC	CARD-14 to bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or
CC	activation of nuclear factor-kappa B (NF-kB). The CARD-14 is useful for
CC	regulating growth and cell death and useful for the treatment of cancer.
CC	It is also useful for the treatment of autoimmune disorders (e.g.,
CC	systemic lupus erythematosus), neurological disorders (e.g., Alzheimer's
CC	and Parkinson's disease, inflammatory disorders, haematological disorders
CC	(e.g., anaemia, myelodysplastic syndromes), myocardial infarctions,
CC	stroke, immune disorders (e.g., Crohn's disease, allergic rhinitis),
CC	cell signalling disorders and certain viral and bacterial infections.
XX	Sequence 1139 AA;
SQ	
Query Match	100.0%; Score 484; DB 22; Length 1139;
Best Local Similarity	100.0%; Pred. No. 5.8e-56;
Matches	92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 EETLWEMESHRRIRVCIPSRLLPYLRQAKVICQDDEEVLHSPRLTNSMRAGHLLD 60
DB	16 EETLWEMESHRRIRVCIPSRLLPYLRQAKVICQDDEEVLHSPRLTNSMRAGHLLD 75
QY	61 LKTRGKGAIAFLESIKFHNDDVYTVTVGLQ 92
DB	76 LKTRGKGAIAFLESIKFHNDDVYTVTVGLQ 107
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ID	AAU01207 standard; Protein; 1147 AA.
XX	AAU01207;
AC	
XX	12-SEP-2001 (first entry)
DT	
XX	Human caspase recruitment domain, CARD-11 polypeptide.
DE	
XX	Human; caspase recruitment domain; CARD-11; Bcl-10; NF-kappaB;
KW	apoptosis; hyperproliferative disorder; autoimmune; neurological;
KM	inflammatory disorder; viral infection; stress-related response.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	Domain
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FT	/note= "CARD domain"
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FT	/note= "Protein kinase C phosphorylation site"
FT	Modified-site
FT	7..10

Ft		/note= "Casein kinase II phosphorylation site"
Ft	Modified-site	100..102
Ft		/note= "Protein kinase C phosphorylation site"
Ft	Modified-site	100..103
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Ft	Modified-site	105..107
Ft		/note= "protein kinase C phosphorylation site"
Ft	Modified-site	106..109
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Ft	Domain	130...431
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Ft	Modified-site	378...381
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Ft	Modified-site	476...479
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Ft	Modified-site	578...561
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Ft	Modified-site	584...587
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Ft	Modified-site	634...637
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Ft	Domain	635...1147
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Ft	Modified-site	638...641
Ft		/note= "Glycosaminoglycan attachment site"
Ft	Modified-site	678...683
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Ft	Modified-site	687...689
Ft		/note= "Protein kinase C phosphorylation site"
Ft	Modified-site	692...695
Ft		/note= "Casein kinase II phosphorylation site"

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 100..103  
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 106..109  
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 175..183  
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 578..581  
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 584..587  
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 587..592  
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 614..637  
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 687..689  
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 692..695  
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# OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 21:36:16 ; Search time 2065.14 Seconds

(without alignments)  
8260.598 Million cell updates/sec

Title: US-10-032-159a-15

Perfect score: 417  
Sequence: 1 atgggggaactgctgcgcag.....ggctcctgtaacccagm 417

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_strs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_strs:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hg\_hum:\*  
31: em\_hg\_inv:\*  
32: em\_hg\_other:\*  
33: em\_hg\_mus:\*  
34: em\_hg\_pln:\*  
35: em\_hg\_rtd:\*  
36: em\_hg\_mam:\*  
37: em\_hg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcgo\_hum:\*  
40: em\_hcgo\_mus:\*  
41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	351	84.2	2621	9 BC018142
2	351	84.2	3662	9 AY032927
3	351	84.2	3766	9 AK091123
4	351	84.2	3931	9 AF322642
5	264.6	63.5	3772	10 AF363457
6	264.6	63.5	3995	10 BC029102
7	212	50.8	55173	2 AC132816
8	212	50.8	144000	9 AC123764
9	212	50.8	182016	9 AC087741
10	212	50.8	187865	2 AC015559
11	212	50.8	207822	2 AC109321
12	205	49.2	55173	2 AC132816
13	188.8	45.3	74301	2 AC137736
14	156	37.4	65608	2 AC132197
15	154.6	37.1	244653	10 AL645911
16	117.8	28.2	3096	6 AX154570
17	117.8	28.2	3908	9 AY032928
18	117.8	28.2	3948	6 AX300499
19	117.8	28.2	3949	6 AX154568
20	117.8	28.2	3949	6 AY028896
21	113	27.1	4085	10 AY135367
22	110.2	26.4	4438	10 AF363456
23	104	24.9	3441	6 AX154573
24	104	24.9	3955	6 AF352576
25	104	24.9	4276	6 AX154571
26	104	24.9	4276	6 AF322641
27	104	24.9	4293	6 AK074049
28	94.4	22.6	765	6 BD150612
29	94.4	22.6	1608	6 AX154567
30	94.4	22.6	2098	6 AX154565
31	94.4	22.6	2132	9 AF311287
32	94.4	22.6	2176	6 BD160313
33	94.4	22.6	2176	9 AK024001
34	92.8	22.3	1836	9 BC008877
35	87.6	21.0	3164	10 BC004692
36	85.2	20.4	1608	6 AX154564
37	85.2	20.4	1879	6 AX154562
38	85.2	20.4	1879	10 AF311288
39	74.8	17.9	96256	9 HS117715
40	74	17.7	239392	2 AC115417
41	74	17.7	245032	2 AC109749
42	70.8	17.0	187446	2 AC124374
43	70.8	17.0	225027	2 AC131725
44	69.2	16.6	161985	10 AL592169
45	69.2	16.6	217819	2 AC026386

## ALIGNMENTS

RESULT 1  
BC018142  
LOCUS  
DEFINITION Homo sapiens, similar to caspase recruitment domain protein 14,  
clone WGC:9539 IMAGE:3847282, mRNA, complete cds.  
ACCESSION BC018142  
VERSION BC018142.1 GI:17390314  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2621)  
AUTHORS Strausberg, R.  
TITLE Direct Submission